

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539,954
Source: PT/10
Date Processed by STIC: 6/30/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/539,954

TIME: 09:07:41

Input Set : A:\Final sequence list-13195-00006-US.txt

Output Set: N:\CRF4\06302005\J539954.raw

3 <110> APPLICANT: Schmitz, Oliver
 4 Puzio, Piotr
 5 Blau, Astrid
 6 Looser, Ralf
 7 Wendel, Birgit
 8 Kamlage, Beate
 9 Plesch, Gunnar
 11 <120> TITLE OF INVENTION: Method for Producing Amino Acids
 13 <130> FILE REFERENCE: 13195-00006-US
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/539,954
 C--> 15 <141> CURRENT FILING DATE: 2005-06-17
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014649
 16 <151> PRIOR FILING DATE: 2003-12-19
 18 <150> PRIOR APPLICATION NUMBER: DE 102 61 188.2
 19 <151> PRIOR FILING DATE: 2002-12-20
 21 <160> NUMBER OF SEQ ID NOS: 26
 23 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1164
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Saccharomyces cerevisiae
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(1164)
 34 <223> OTHER INFORMATION: Threonine aldolase
 36 <400> SEQUENCE: 1
 37 atg act gaa ttc gaa ttg cct cca aaa tat atc acc gct gct aac gac 48
 38 Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
 39 1 5 10 15
 41 ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc 96
 42 Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
 43 20 25 30
 45 gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac 144
 46 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
 47 35 40 45
 49 acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca 192
 50 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
 51 50 55 60
 53 ggt ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga 240
 54 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
 55 65 70 75 80
 57 act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct 288
 58 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala

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59	85	90	95	
61 cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg				336
62 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala				
63	100	105	110	
65 atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa				384
66 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu				
67	115	120	125	
69 gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc				432
70 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala				
71	130	135	140	
73 ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat				480
74 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr				
75	145	150	155	160
77 cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt				528
78 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly				
79	165	170	175	
81 ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa				576
82 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln				
83	180	185	190	
85 tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc				624
86 Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser				
87	195	200	205	
89 atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt				672
90 Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val				
91	210	215	220	
93 ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa				720
94 Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln				
95	225	230	235	240
97 ggt ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta				768
98 Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val				
99	245	250	255	
101 aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg				816
102 Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu				
103	260	265	270	
105 gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag				864
106 Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu				
107	275	280	285	
109 tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga				912
110 Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg				
111	290	295	300	
113 atg gac cca gat gtc ctt gtt aag aag ggt ttg aag tac aac gtt aag				960
114 Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys				
115	305	310	315	320
117 cta atg ggt ggt aga gtc tcg ttc cac tat caa gtc acc aga gat act				1008
118 Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr				
119	325	330	335	
121 ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa				1056
122 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys				
123	340	345	350	

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```

125 gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa      1104
126 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
127      355      360      365
129 tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc      1152
130 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
131      370      375      380
133 tac aaa tac tga      1164
134 Tyr Lys Tyr
135 385
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 387
140 <212> TYPE: PRT
141 <213> ORGANISM: Saccharomyces cerevisiae
143 <400> SEQUENCE: 2
144 Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
145 1      5      10      15
147 Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
148      20      25      30
150 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
151      35      40      45
153 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
154      50      55      60
156 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
157 65      70      75      80
159 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
160      85      90      95
162 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
163      100      105      110
165 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
166      115      120      125
168 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
169      130      135      140
171 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
172 145      150      155      160
174 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
175      165      170      175
177 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
178      180      185      190
180 Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
181      195      200      205
183 Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
184      210      215      220
186 Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
187 225      230      235      240
189 Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
190      245      250      255
192 Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
193      260      265      270
195 Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu

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196          275          280          285
198 Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
199          290          295          300
201 Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
202 305          310          315          320
204 Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
205          325          330          335
207 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
208          340          345          350
210 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
211          355          360          365
213 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
214          370          375          380
216 Tyr Lys Tyr
217 385
220 <210> SEQ ID NO: 3
221 <211> LENGTH: 376
222 <212> TYPE: PRT
223 <213> ORGANISM: Canola
225 <400> SEQUENCE: 3
226 Gly Cys Phe Ala Cys Tyr Leu Val Gly Gly Phe Ser Val Gln Glu Lys
227 1          5          10          15
229 Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro
230          20          25          30
232 Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp
233          35          40          45
235 Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala
236          50          55          60
239 Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
240 65          70          75          80
242 Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu
243          85          90          95
245 Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly
246          100          105          110
248 Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp
249          115          120          125
251 Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro
252          130          135          140
254 Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn
255 145          150          155          160
257 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp
258          165          170          175
260 Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp
261          180          185          190
263 Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp
264          195          200          205
266 Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
267          210          215          220
269 Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile

```

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```

270 225          230          235          240
272 Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
273          245          250          255
275 Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val
276          260          265          270
278 Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly
279          275          280          285
281 Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr
282          290          295          300
284 Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
285 305          310          315          320
287 Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
288          325          330          335
290 Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
291          340          345          350
293 Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
294          355          360          365
296 Gly Val Gln Lys Glu Met Gly Asn
297          370          375

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300 <210> SEQ ID NO: 4

301 <211> LENGTH: 115

302 <212> TYPE: PRT

303 <213> ORGANISM: Soybean

305 <400> SEQUENCE: 4

```

306 Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val
307 1          5          10          15
309 Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
310          20          25          30
312 Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Val Leu
313          35          40          45
315 Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
316          50          55          60
318 Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
319 65          70          75          80
321 Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
322          85          90          95
324 Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
325          100          105          110
327 Thr Leu Gly
328          115

```

331 <210> SEQ ID NO: 5

332 <211> LENGTH: 127

333 <212> TYPE: PRT

334 <213> ORGANISM: Rice

336 <220> FEATURE:

337 <221> NAME/KEY: misc_feature

338 <222> LOCATION: (1)..(127)

339 <223> OTHER INFORMATION: unknown or other

341 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 06/30/2005

PATENT APPLICATION: US/10/539,954

TIME: 09:07:42

Input Set : A:\Final sequence list-13195-00006-US.txt

Output Set: N:\CRF4\06302005\J539954.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 4

Seq#:7; Xaa Pos. 5

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/539,954**

DATE: 06/30/2005

TIME: 09:07:42

Input Set : **A:\Final sequence list-13195-00006-US.txt**

Output Set: **N:\CRF4\06302005\J539954.raw**

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0